













Author Correction: Pan-cancer image-based detection of clinically actionable genetic alterations

Jakob Nikolas Kather , Lara R. Heij, Heike I. Grabsch , Chiara Loeffler, Amelie Echle, Hannah Sophie Muti, Jeremias Krause, Jan M. Niehues, Kai A. J. Sommer, Peter Bankhead, Loes F. S. Kooreman, Jefree J. Schulte , Nicole A. Cipriani , Roman D. Buelow , Peter Boor, Nadina Ortiz-Brüchle , Andrew M. Hanby, Valerie Speirs , Sara Kochanny, Akash Patnaik, Andrew Srisuwananukorn, Hermann Brenner, Michael Hoffmeister, Piet A. van den Brandt , Dirk Jäger, Christian Trautwein, Alexander T. Pearson  and Tom Luedde 

Correction to: *Nature Cancer* <https://doi.org/10.1038/s43018-020-0087-6>, published online 27 July 2020.

In the version of this article initially published, the sample size ($n = 794$) was incorrect in Fig. 2f and Extended Data Fig. 4a,e; the correct sample size is ' $n = 397$ '. The sample size ($n = 826$) was also incorrect in Fig. 2h and Extended Data Fig. 4q,u; the correct sample size is ' $n = 413$ '. Also, the values in Supplementary Table 2, row 'TCGA-HNSC', column 'Quality OK and tumor on slide' (424, 424) were incorrect; the correct values are '457, 439'. The errors have been corrected in the HTML and PDF versions of the article.

Published online: 3 November 2020

<https://doi.org/10.1038/s43018-020-00149-6>

© The Author(s), under exclusive licence to Springer Nature America, Inc. 2020